

1. (Amended) An isolated nucleic acid molecule from *Magnaporthe grisea* comprising a segment of chromosome 1 approximately 1 kb in size and containing at least one open reading frame, the segment conferring [that confers] rice cultivar CO39-specific avirulence to fungal plant pathogens that contain the nucleic acid.

2. (Amended) The nucleic acid molecule of claim 1, having a nucleotide sequence at least 60 % identical to SEQ ID NO:1, the identity being calculated by hybridization with SEQ ID NO:1 under conditions derived from a formula of:

$$T_m = 81.5^{\circ}\text{C} + 16.6\text{Log} [\text{Na}^+] + 0.41(\% \text{ G+C}) - 0.63 (\% \text{ formamide}) - 600/\text{\#bp in duplex [which is AVR1-CO39].}$$

4. (Amended) The nucleic acid molecule of claim 1, which encodes a polypeptide [having the features of a polypeptide] comprising a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8.

7. (Amended) A non-mammalian cell transformed with the recombinant DNA molecule of claim 6.

8. (Amended) The cell of claim 7, wherein said cell is either [selected from the group consisting of] bacterial [cells], fungal [cells], insect, or [cells and] plant [cells].

9. (Amended) The [transformed] cell of claim 8, which is an epiphytic bacterial cell.

10. (Amended) A transgenic plant regenerated from the [transformed] cell of claim 8.

11. (Amended) An isolated nucleic acid molecule comprising [having] a sequence selected from the group consisting of:

- a) [part or all of] SEQ ID NO:1;
- b) an allelic variant of an isolated nucleic acid molecule comprising[part or all of] SEQ ID NO:1;

an open reading frame located between nucleotides 443 and 676;
an open reading frame located between nucleotides 582 and 850;
an open reading frame located between nucleotides 753 and 858;
an open reading frame located between nucleotides 885 and 1047;
an open reading frame on the complementary strand of SEQ ID
NO:1 located between nucleotides 757 and 561;
an open reading frame on the complementary strand of SEQ ID
NO: 1 located between nucleotides 419 and 312 [a natural mutant of SEQ ID
NO:1];
 d) an allelic variant of the segment of SEQ ID NO:1;
 e) a sequence that hybridizes with any of the sequences of a) - d) or its
complement under high stringency conditions [hybridizing with part or all of
 SEQ ID NO:1 or its complement and encoding a polypeptide substantially the same as
 any of the polypeptides encoded by SEQ ID NO:1]; and
 f) a sequence encoding [part or all of] a polypeptide having an amino
acid sequence comprising any one of [selected from the group consisting of] SEQ ID
NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID
NO:7 or [and] SEQ ID NO:8.

14. (Amended) A non-mammalian cell transformed with the recombinant DNA molecule of claim 13.

15. (Amended) The cell of claim 14, wherein said cell is either
[selected from the group consisting of] bacterial[cells], insect, yeast, or [cells and
]plant [cells].

25. (Amended) A transgenic epiphytic bacterium that expresses a portion of an AVR1-CO39 gene which confers[effective to confer] rice cultivar CO39-
specific avirulence to microorganisms expressing the gene.

26. (Amended) The transgenic epiphytic bacterium of claim 25[24],
which expresses the amino acid sequence of SEQ ID NO:4[ORF3 of SEQ ID NO:1], or
an allelic variant thereof[a functional equivalent].

REMARKS

Printed Name of Applicant